

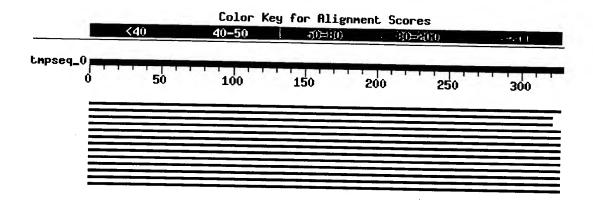
TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCCTGACAC
GATTCTTTGCCTTCCACTTCATCCTTCCATTTATCATCTCAGC
TCTAGCAGCAGTCCACCTCCTATTCCTTCACGAGACAGGATCT
AACAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCAT
TCCACCCATACTACACAATCAAAGATATCCTGGGCCTTCTAGT
ACTAATCCTAGCACTCATACTACTCGTCCTATTCTCACCAGAC
CTGTTAGGAGACCCCGATAACTACATCCCTGCCAACCCTCTAA
ATACCCCTCCCCATATCAAGCCTGAAT

Figure 1 a

Sequence of cytochrome b gene (328 bp) revealed from biological material of unknown origin i.e. 'adil.flesh' using primers 'mcb398' and 'mcb869'

Homology search in 'nr' database using 'BLAST'

http://www.ncbi.nlm.nih.gov/BLAST/



Sequences producing significant alignments:	Score (bits)	E Value
gb AY005809.1 <i>Panthera pardus</i> cytochrome b gene, partial c gb AF053054.1 AF053054 <i>Panthera tigris sumatrae</i> isolate Su1 gb AF053053.1 AF053053 <i>Panthera tigris tigris</i> isolate B7 mi gb AF053050.1 AF053050 <i>Panthera tigris corbetti</i> isolate C2 gb AF053049.1 AF053049 <i>Panthera tigris corbetti</i> isolate C1	603 527 527 476 476	e-170 e-147 e-147 e-132 e-132

200

Selection of reference animals based on above information and further analysis using primers 'mcb398' and 'mcb869'

Multiple sequence alignments using 'Autoassembler'

	225	. 250	275	200	
	-CTAG~TGCTAAT~C-	IA:CaC~ICAI~ACT.AC.T=G	T C CLATICISISCE	300	325
		· · · · · · · · · · · · · · · · · · ·	T~~C~CTATTCTEACCAGACCTatTaGG	g~GACCCC~GAŧAACTAcAŧ~C~CCc~	GCCAACCC~T(
gz2L	-CTAG-TACTAAT-CT	TAGEAC-TEAT-ACT AC TEC	T 6 67177777	 	
bhz251	CTAG-TACTAAT-CC	TAACAC-TCAT-ACT-AC-TCG	TC-CTATTCTCACCAGACCTGTT-GG	GAGACCCC-GATAACTACAT-C-CCC-	GCCAACCE-TI
dz14si	·CTAG-TACTAAT-CC	TAACAC-TCAT-ACT-AC-TCG	T - C CTATTCTCACCAGACCTATTAGG	u-ballle-GATAACTACAT-C-CCC-	GCCAACCC-TI
chimss	\$ \-TTCCT-TTT -cc	TC-CTTATCCT-AATGACAT	TARCICIATION	U-UALULL-UA!AACTACAT-C-CCC-	·GCCAACCC-Ti
gz22ci	·CTAG-TICTAATTCT	-AGCGC-TCAC-ACT-AC-TTG	TAACACTATTCTCACCAGACCTCCTGGG TT-CTATTCTCCCCAGACCTACTAGG.	C-GAT-CCAGACAACTATAC-CCTA	GCTAACCCCC
sbz22a	U-CTAG-TACTAAT-CT	TAACAC-TCAT-ACT-AC-TCG	TAACACTATICTCACCAGACCTACTAGG.	A-GA-CCCTGACAA-T-TACACTCCC-	GCCAACCC-TI
humsk	VCTTC-T-CTT-CC	TT-CTC-TCCTTAATGACAT-	TAACACTATTCTCACCAGACCTATTAGG. TAACACTATTCTCACCAGACCTCCTAGGI	A-GATCCC-GACAACTATAC-C-CCC-	GCCAATCC-TI
bhz20v	M-CTAG-TACTAAT-CC	TAACAC-TCAT-ACT-AC-TCG	THACACTATICICACCAGACCTCCTAGG TC-CTATICICACCAGACCTATTAGGI TC-CTATICICACCAGACCTATTAGGI	L-GAC-CCAGACAATTATAC-CCTA	GCCAACCCCT
gz3L	-CTAG-TACTAAT-CT	TAGCAC-TCAT-ACT-AC-TCG	TC-CTATTCTCACCAGACCTATTAGGI TC-CTATTCTCACCAGACCTGTT-GGA	G-GALCLE-GATAACTACAT-C-CCC-	GCCAACCC-TI
gz1L	-CTAG-TACTAAT-CC	TAGCAC-TCAT-ACT-AC-TCG	TC-CTATICICACCAGACCTGTT-AGG TC-CTATICICACCAGACCTGTT-AGG	GAGACCCC-GATAACTACAT-C-CCC-	GCCAACCC-Ti
adil.fles	SHCTAG-TACTAAT-CC	TAGCAC-TCAT-ACT-AC-TCG	TC-CTATTCTCACCAGACCTGTT-AGG TC-CTATTCTCACCAGACCTGTT-AGG	UAGALLEE-GATAACTACAT-C-CCT-	GCCAACCC-TI
				UAUALLLL-GATAACTACAT-C-CCT-	6CC44CCC_TI

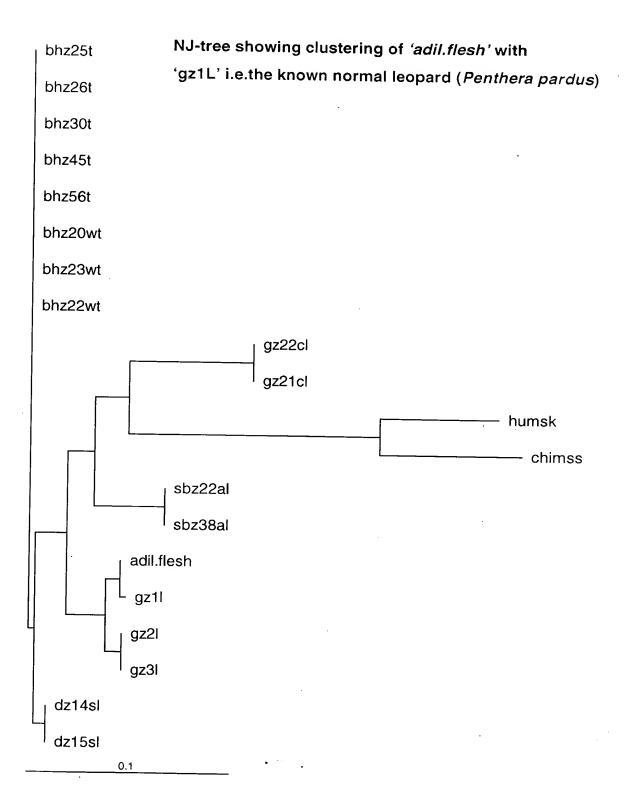


Figure 1c

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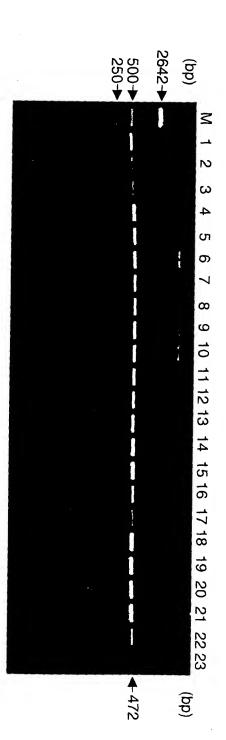


Figure 2

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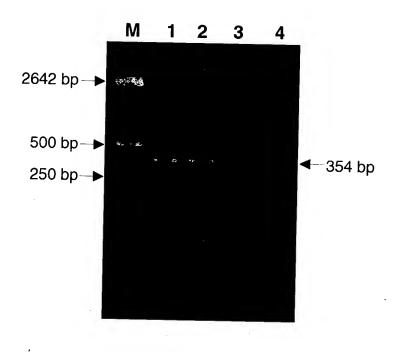


Figure 3

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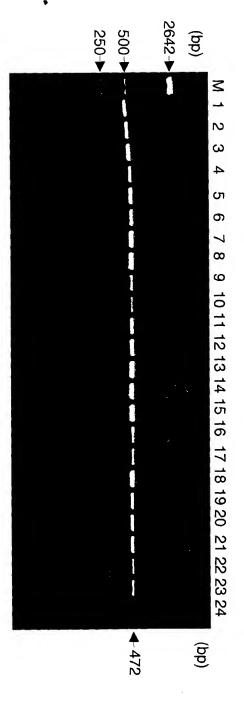


Figure 4